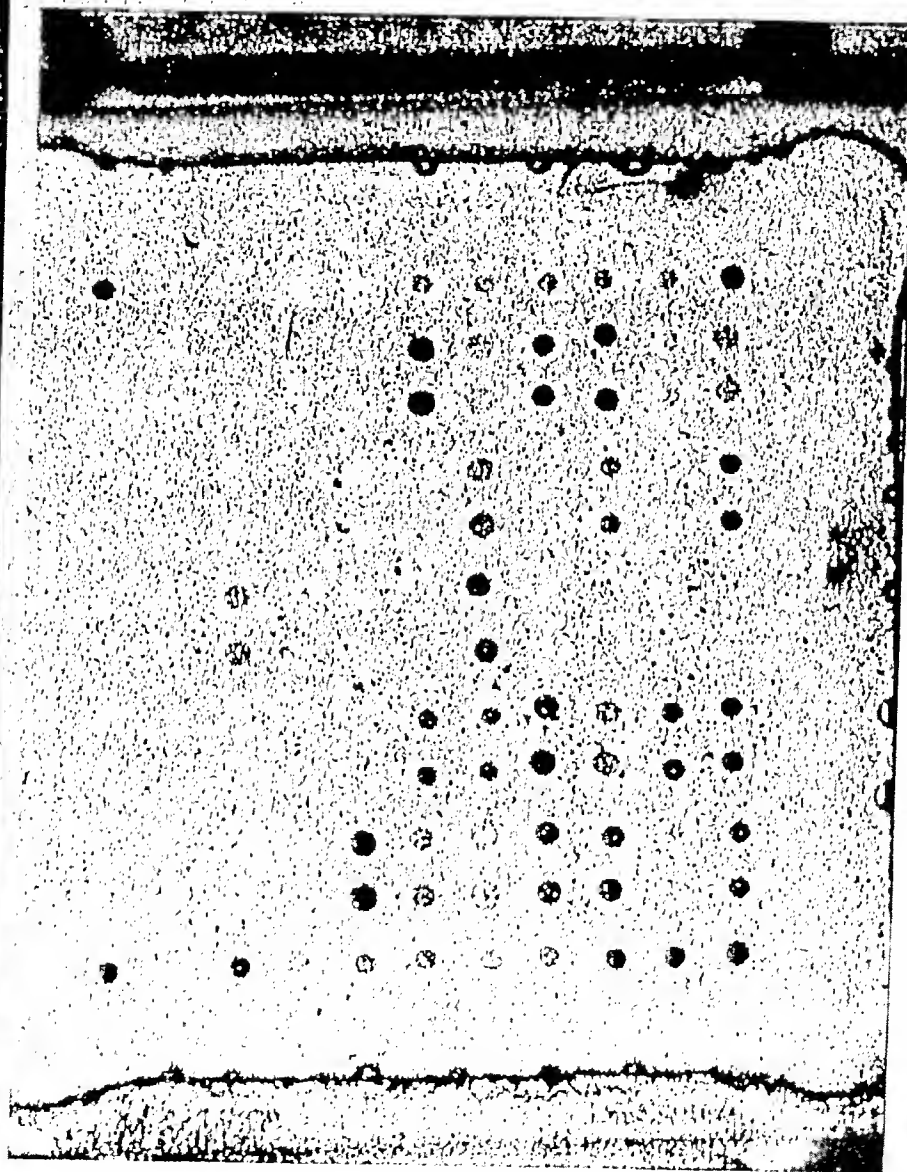


FIGURE 1

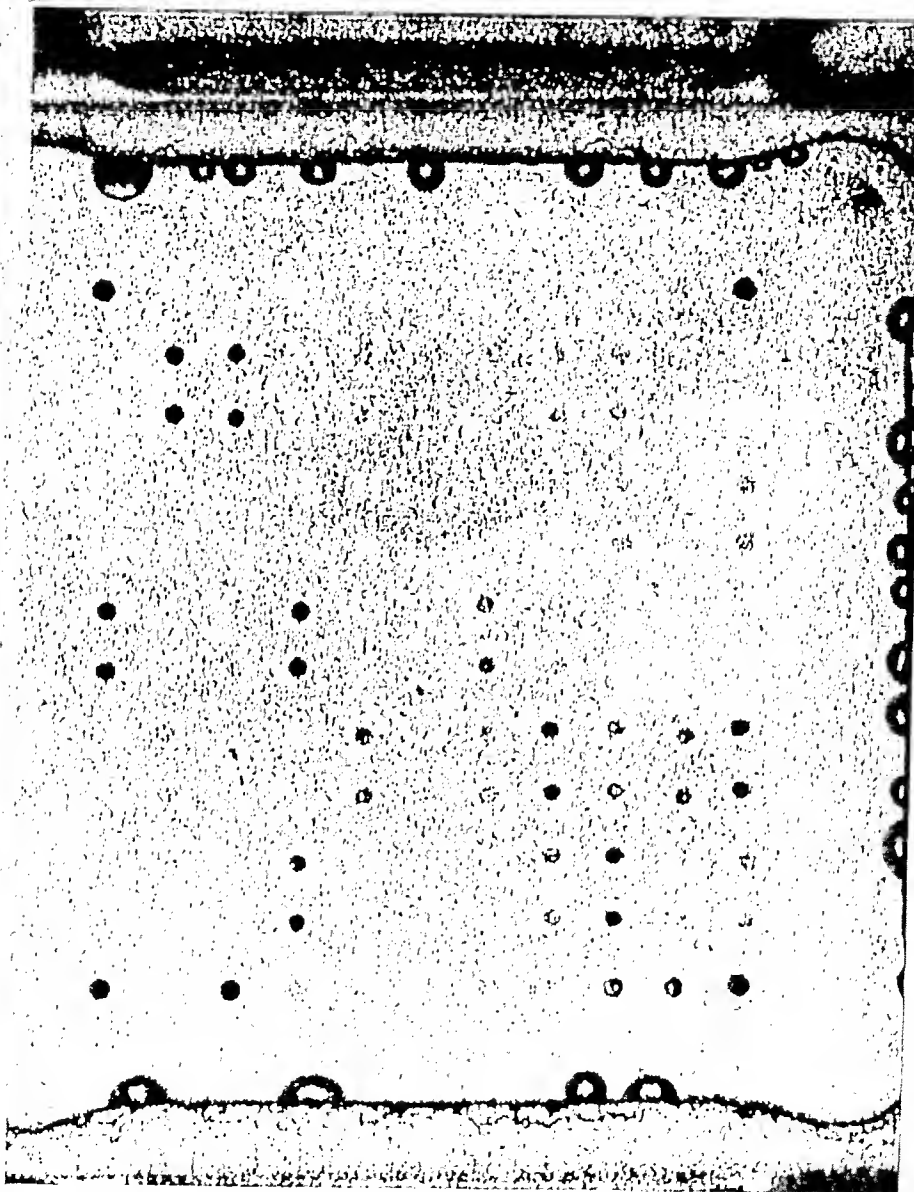
P. aeruginosa AT-Chip



ZW117

FIGURE 2

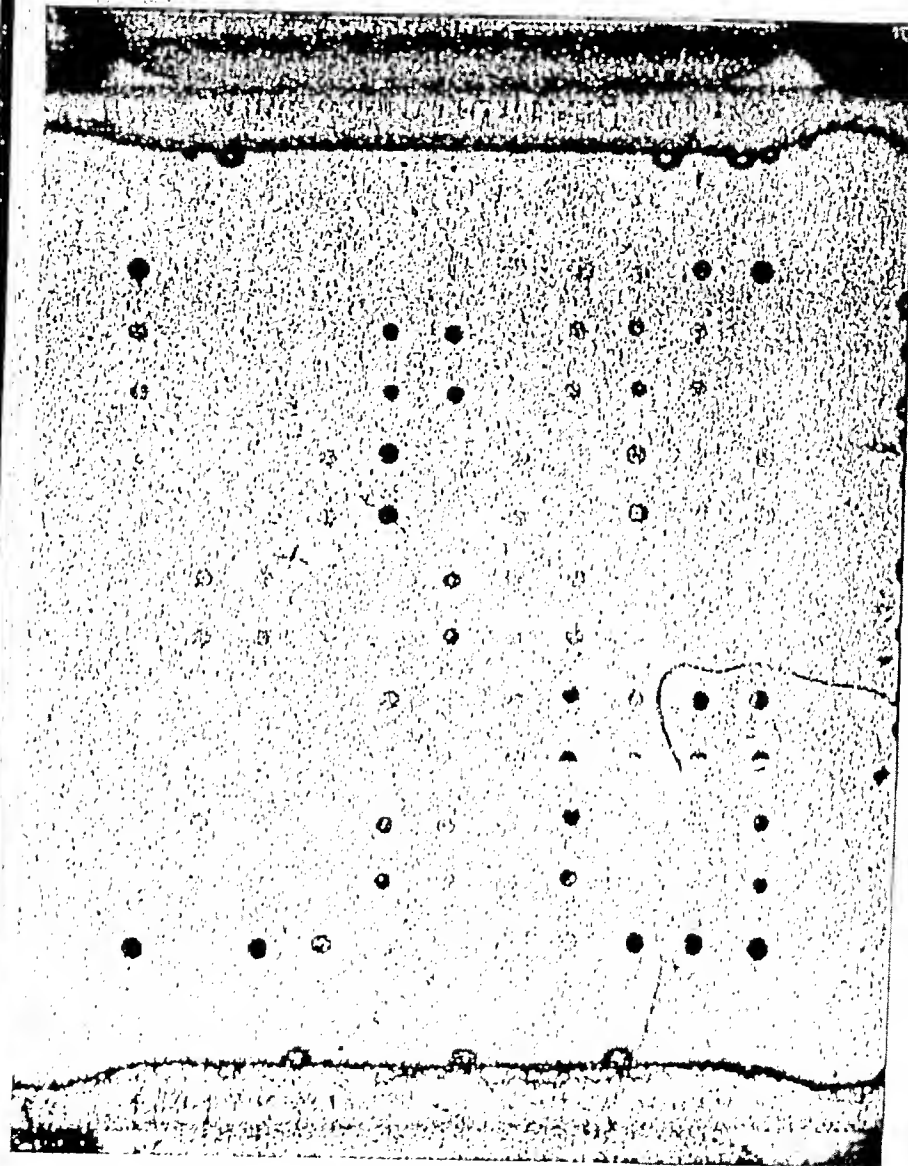
P. aeruginosa AT-Chip



RP17

FIGURE 3

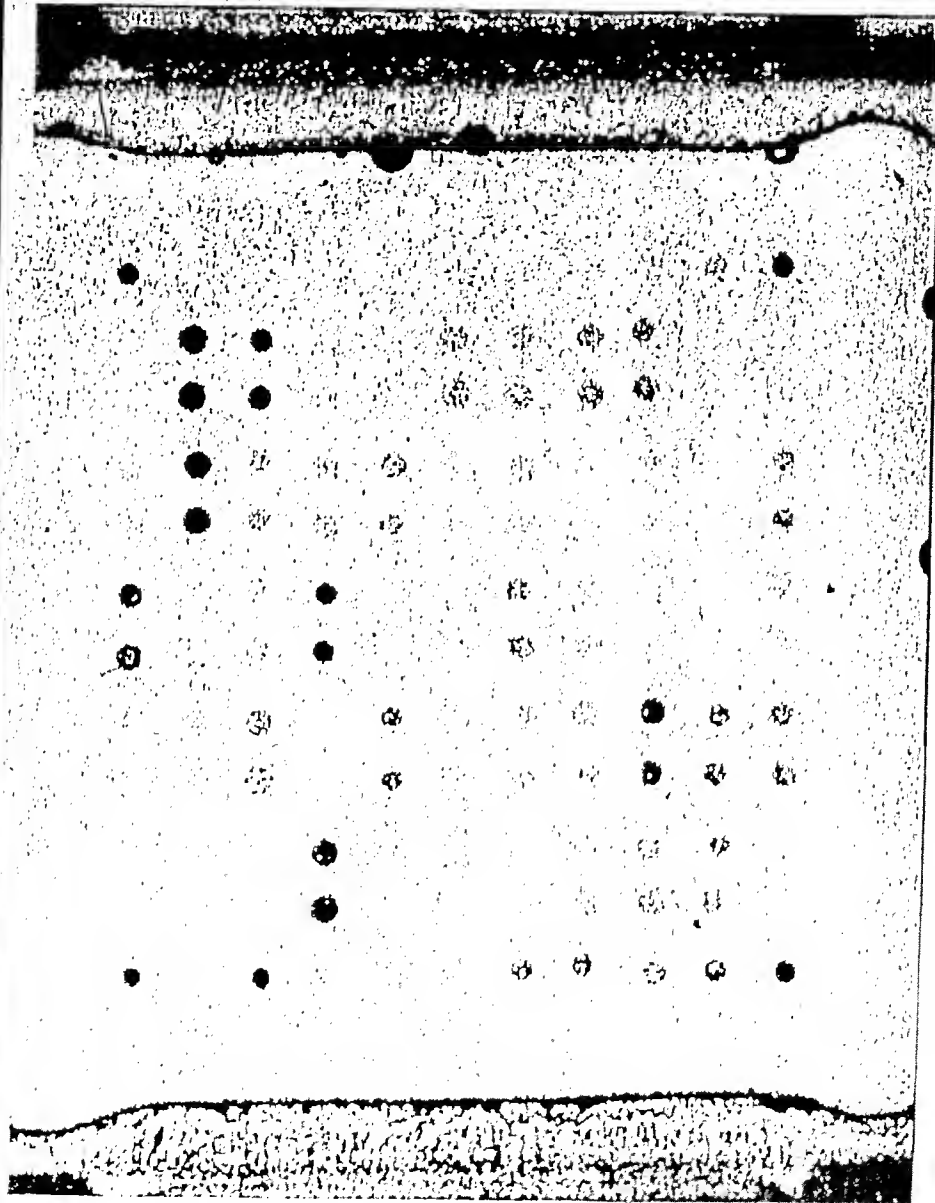
P. aeruginosa AT-Chip



TB

FIGURE 4

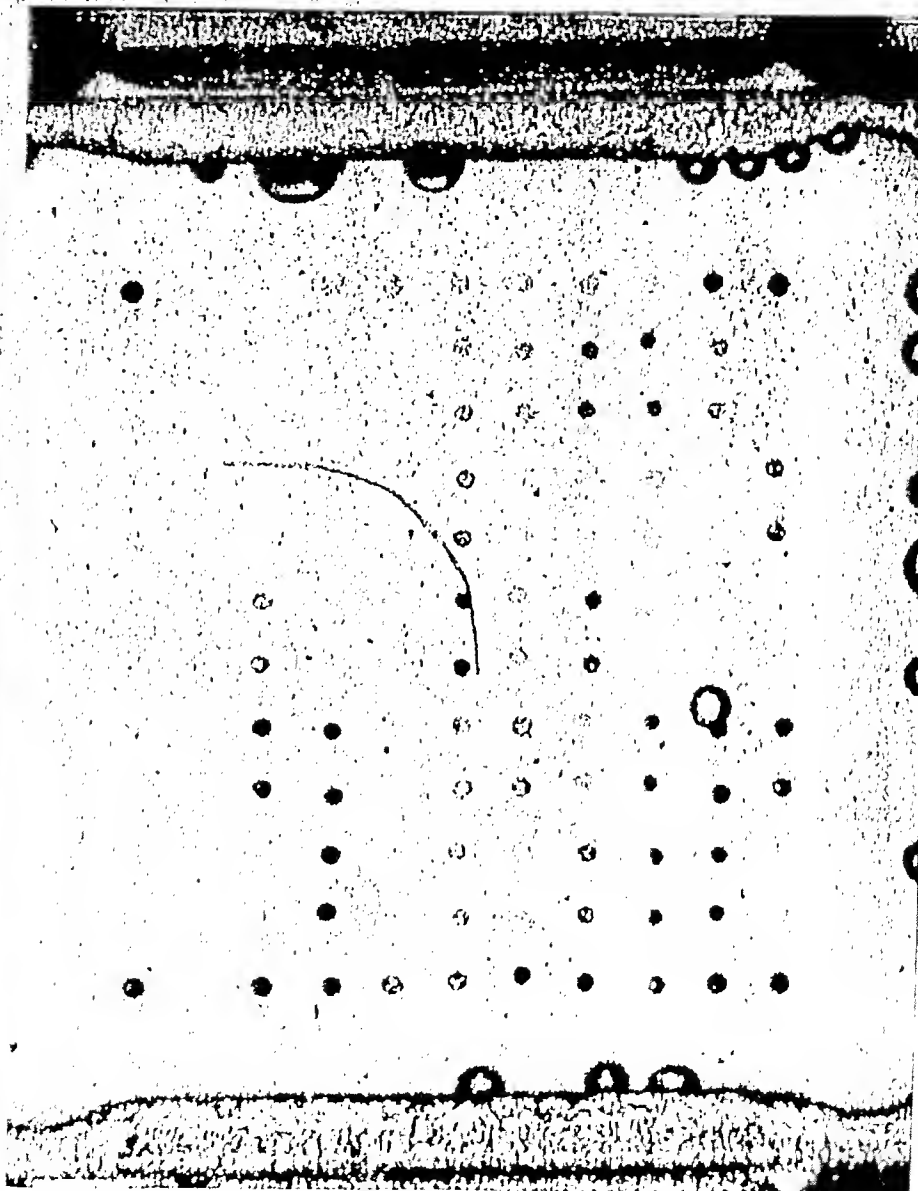
P. aeruginosa AT-Chip



SG17M

FIGURE 5

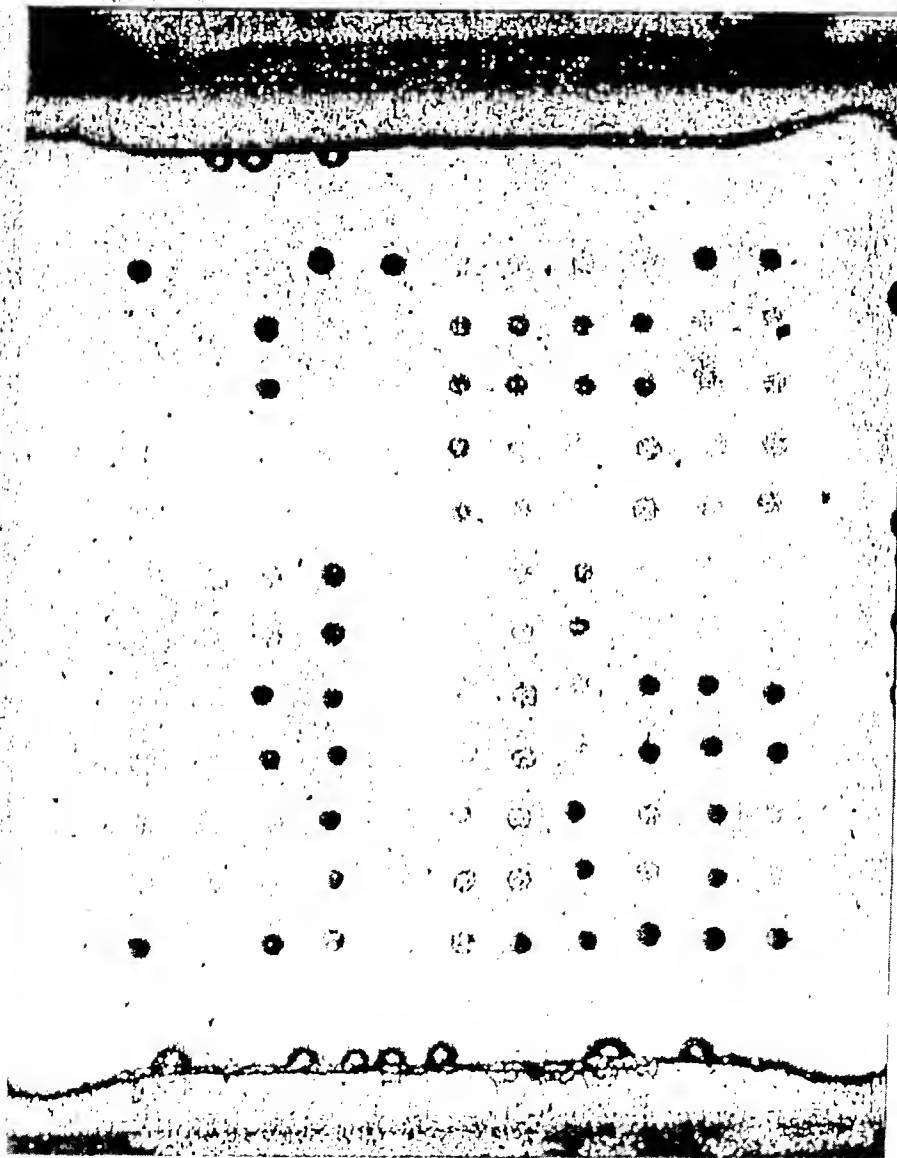
P. aeruginosa AT-Chip



BST85

FIGURE 6

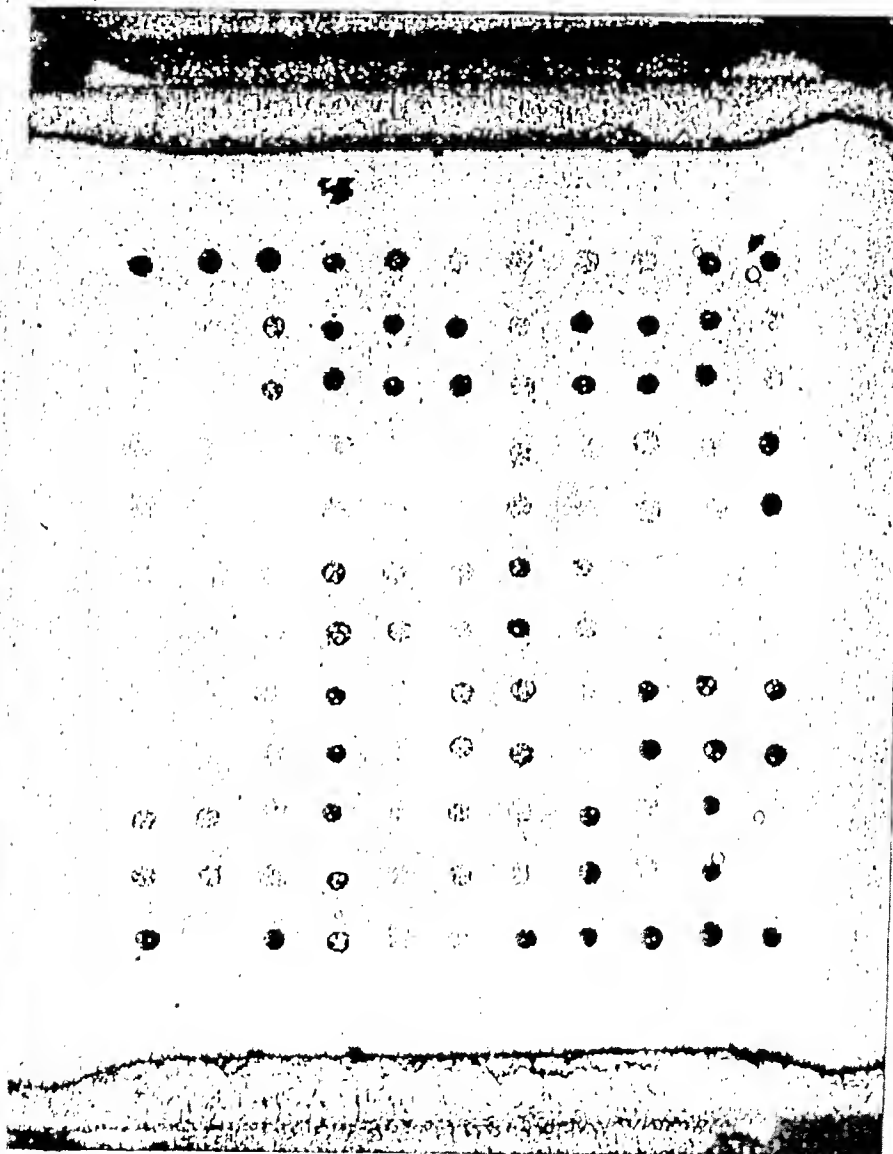
P. aeruginosa AT-Chip



AL5846

FIGURE 7

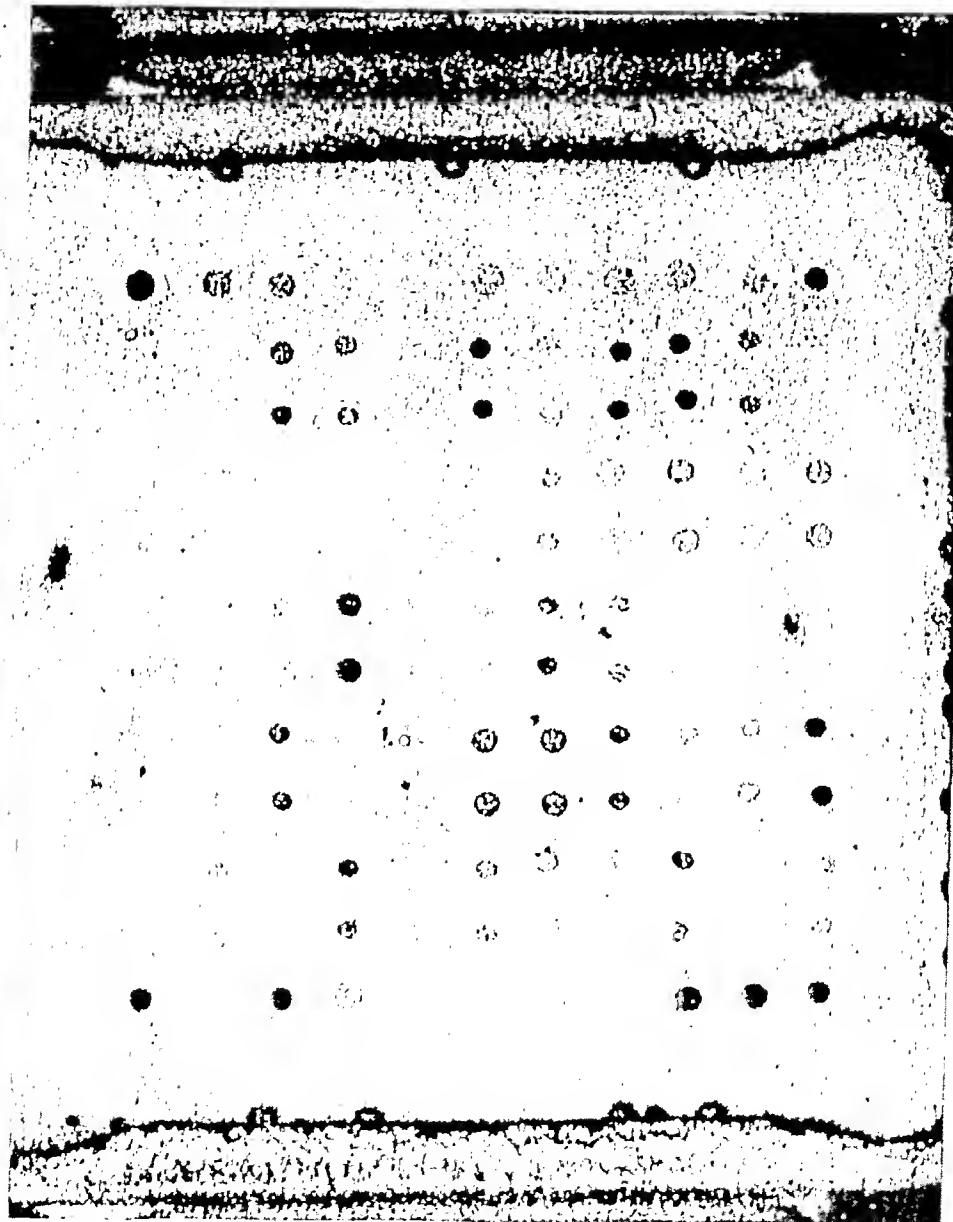
P. aeruginosa AT-Chip



PT12

FIGURE 8

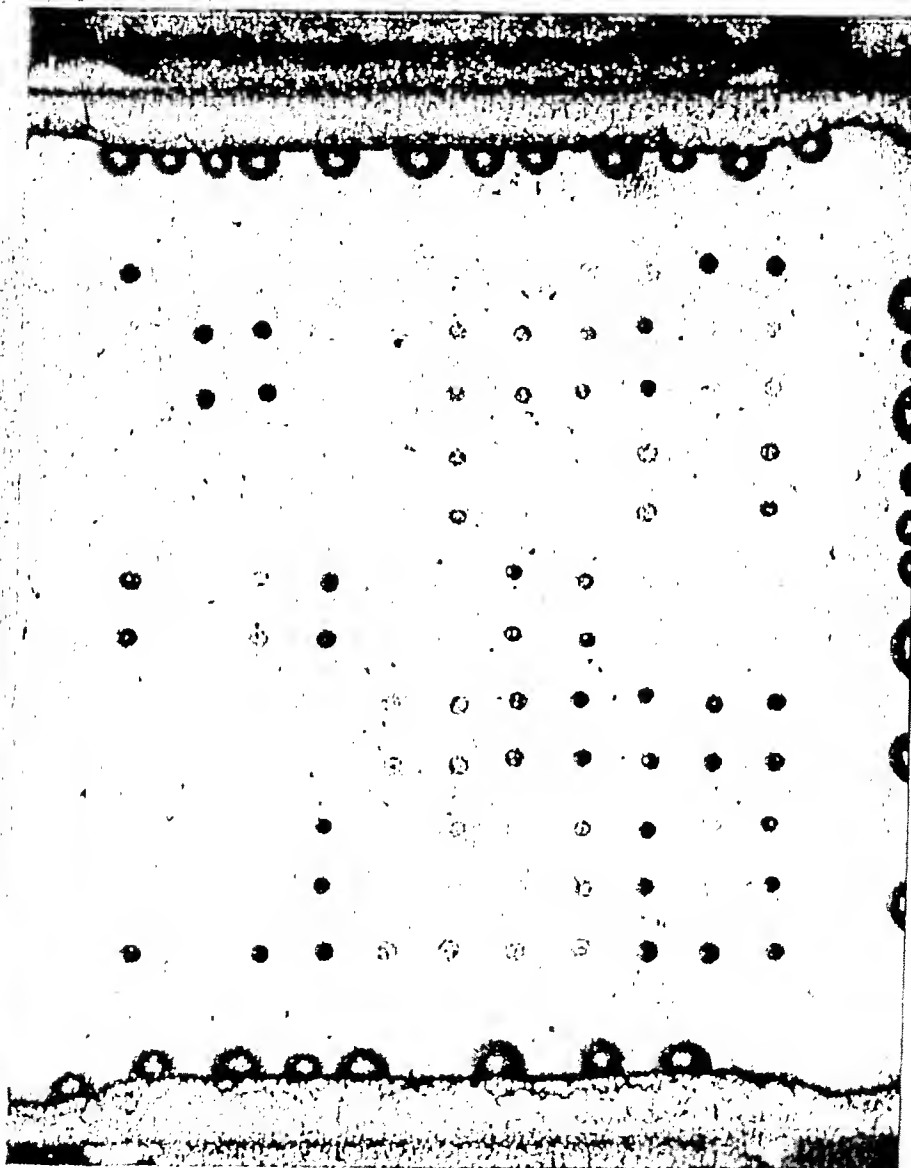
P. aeruginosa AT-Chip



PT20

FIGURE 9

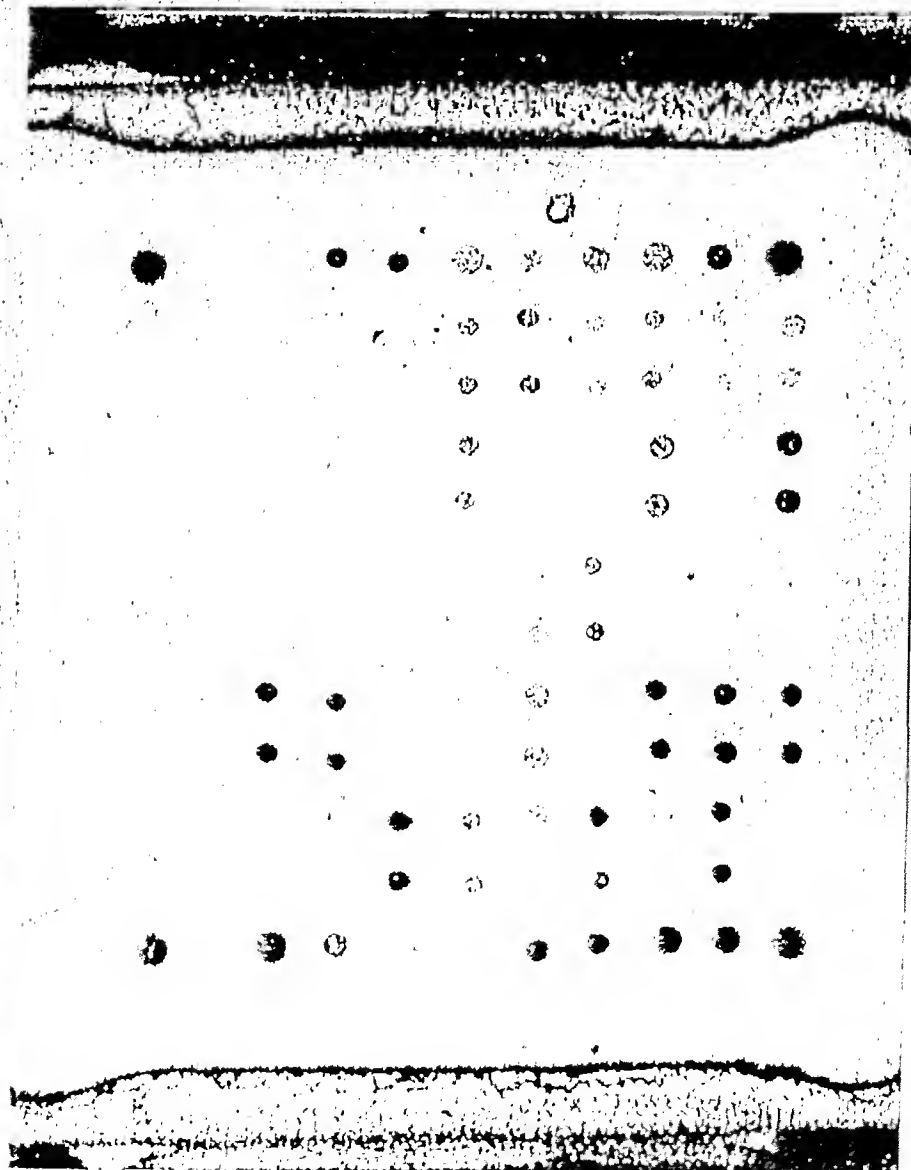
P. aeruginosa AT-Chip



ZW79

FIGURE 10

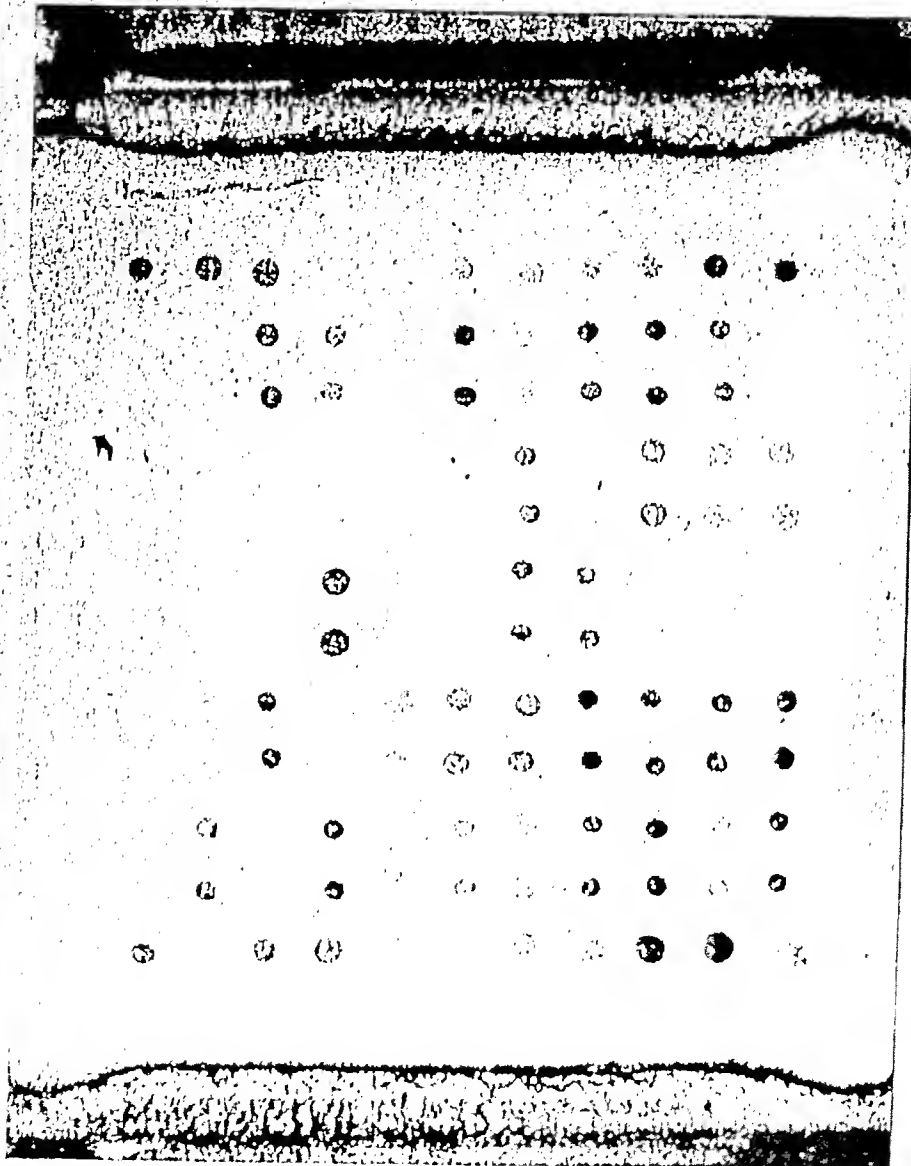
P. aeruginosa AT-Chip



ZW85

FIGURE 11

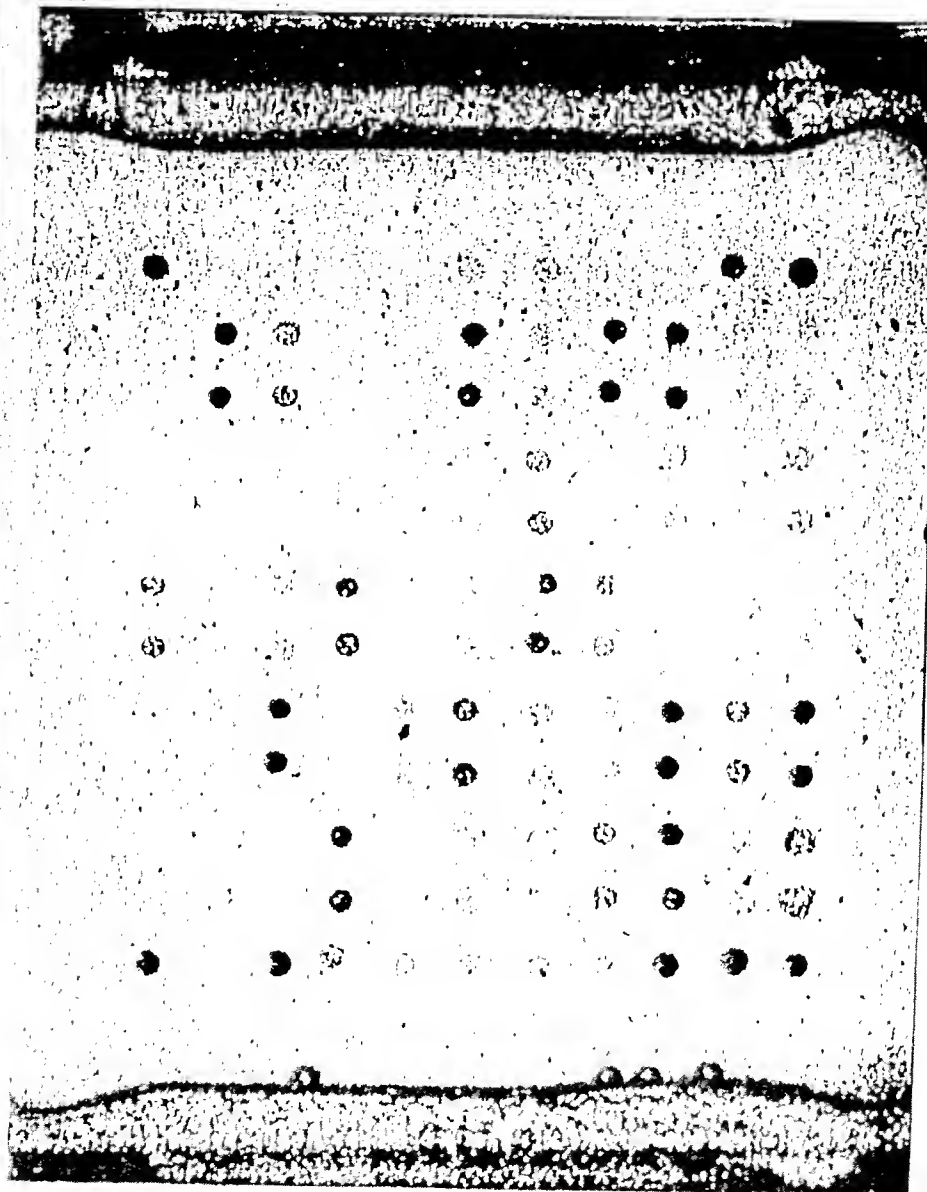
P. aeruginosa AT-Chip



2813A

FIGURE 12

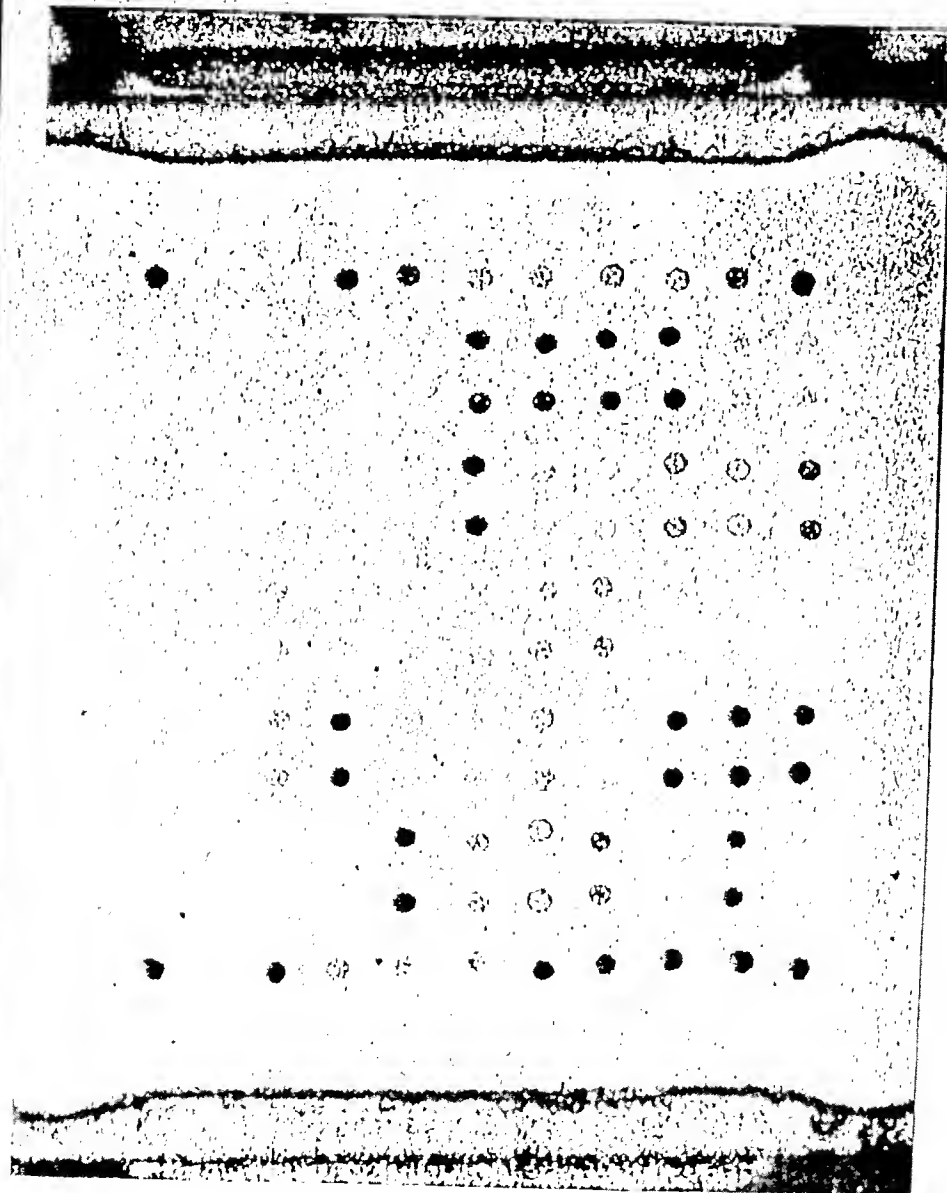
P. aeruginosa AT-Chip



KB1-85

FIGURE 13

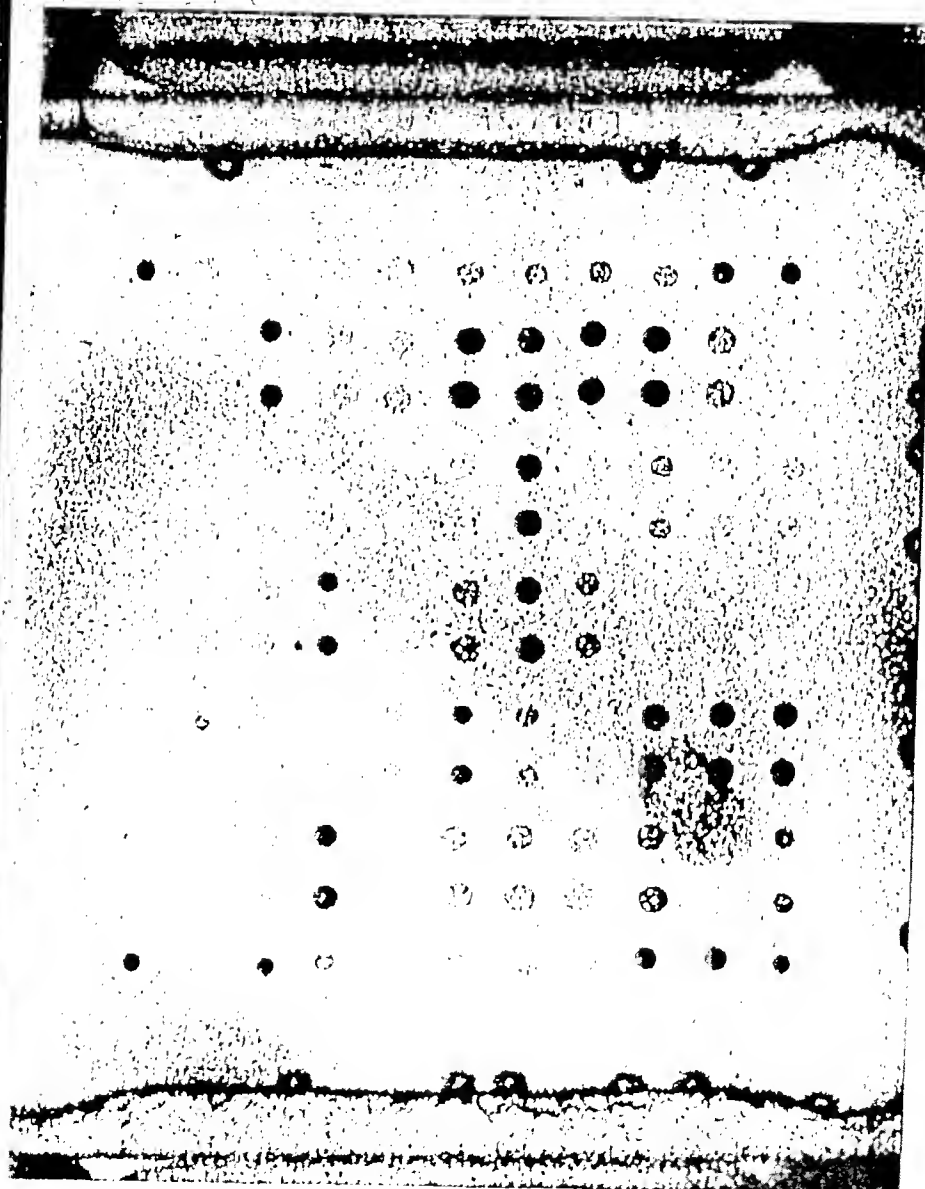
P. aeruginosa AT-Chip



ZW98

FIGURE 14

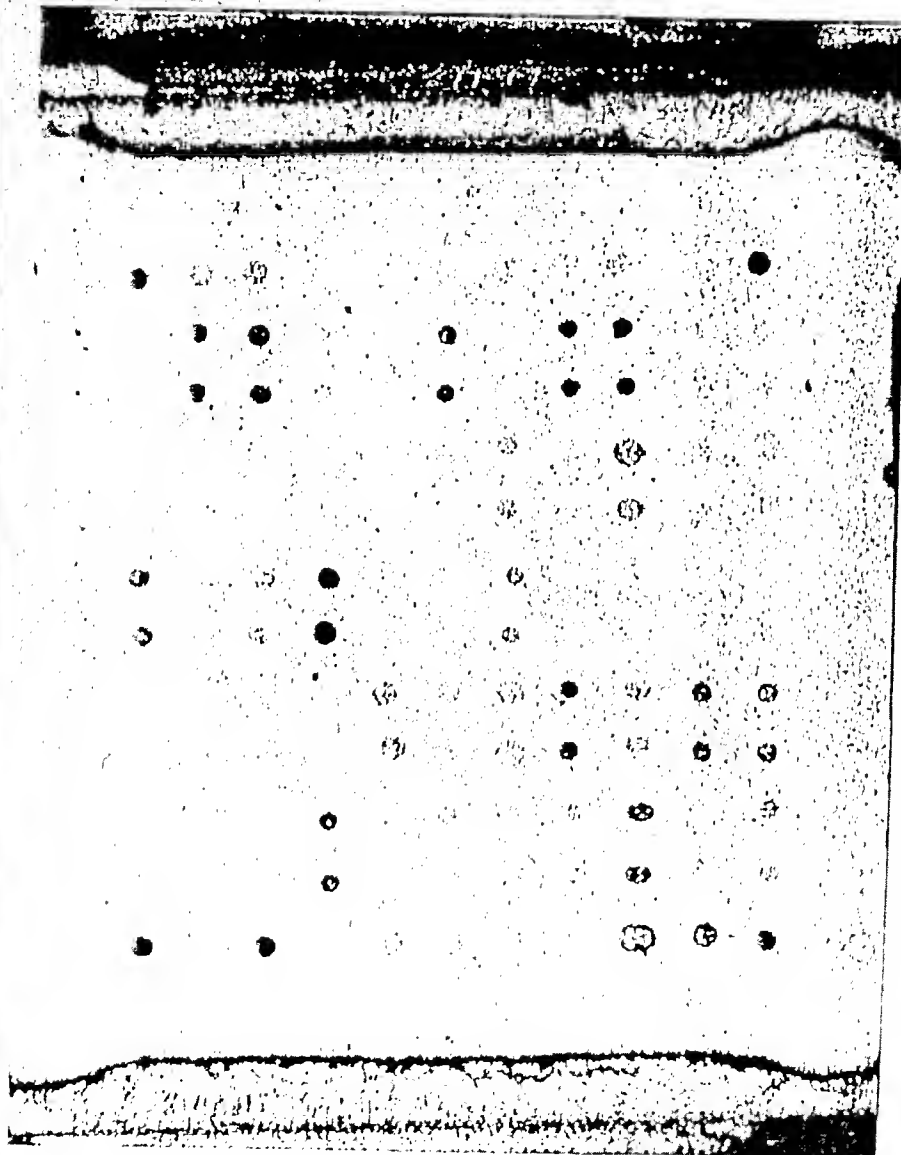
P. aeruginosa AT-Chip



641HD

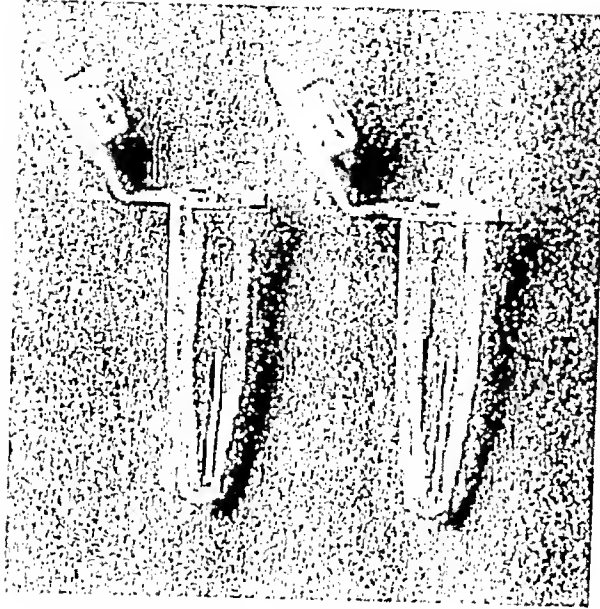
FIGURE 15

P. aeruginosa AT-Chip



ATCC15522

FIGURE 16



REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 17A

47-1/23
ACGCGGATGTCCTGGATTGG

47-1/39
CTGAAGAAGGGGCGCTACGCG

47-2/22
GCGTACCGGGCAAGGTGATAG

47-2/52
CTCGGTGAAACATCGGGAGGG

C45/18
TCATCCAGCAAGCCATTGCGC

C45/60a
GGAGTCGCTTTCCGCCATCG

C45/60b
TGGAGTCGCTTTCCGCCATCG

C46/15
AAGGGCGTTTCACGCTGACGC

C46/22
ATCCGGAAGGGCGTTTCACG

C46/88
TCCACACCTCAGACTTCGGCG

C47-1/43
TATTGACGACCTACCGCGCGC

C47-2/56a
GCAACTGATGTTGCCCCAGC

C47-2/56b
CGCAACTGATGTTGCCCCAGC

C47-2/59
ACACGCAACTGATGTTGCCCC

CIS-4/36
TGTCCCGGCTCAGTTCAACG

CIS-4/50
AACACCTTGGCGTTTGTCCC

CIS-4/51
GCAACACCTTGGCGTTTGTCC

CIS-5/4
TCAAGCTCGTTGTGGACCGC

CIS-5/48
GTTACGACGGCGTGCTGTCGG

CSP-1/39a
ACGCAACGTATTGCGCGACCC

CSP-1/39b
CGCAACGTATTGCGCGACCC

REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 17B

fliAT/28
AGCTGATGGTATCGCCGTCGC

fliAT/72
CTAGTGATCGCACCGGAGCC

oriC/20
AGCCTCGACACCGGTTCTCG

oriC/54
TCGTTTCATCCCCAGGCTTCG

oriC/59
ACCATCTCGTTCATCCCCAGG

oprL/53
TTCTGAGCCCAGGACTGCTCG

oprL/65
TCGACGCGACGGTTCTGAGCC

fliCb/36
TGACGTTCTCGCCGGTAGCG

fliCb/65
CAGTAGCGGTACCGGTCTGCG

fliCb/66
CAGTAGCGGTACCGGTCTGC

alkAG/27
TTCTCGCCGGCATAGTAGGC

alkGA/32

alkGA/51
CGAGGACGAGGCATCTTCCGG

citAG/4
GCAGGTAGCAGGTTTCCAGG

citAG/46
AACTGTTCCCTTCTGCGCGGCG

citGC/8
TGATCGGCTTGGTCTCGCAGG

citGC/11
GCTGATCGGCTTGGTCTCGC

citGC/75
GAGGCGTTCTGCTCGTGGTCG

oprI/12
TTTTTCCAGCATGCGCAGGG

oprI/17
GCTGGCTTTTCCAGCATGCG

oprI/22
TTGCGGCTGGCTTTTCCAGC

REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 17C

am7CA/1
TTGGGATAGTTGCGGTTGGC

am7CA/27
CGTAGGCGATCTTCACCCGC

am7CA/29
TGGCGTAGGCGATCTTCACCC

am3CT/21
GGCGAGATAGCCGAACAGGC

am3CT/22
GCGGCGAGATAGCCGAACAGG

am3CT/69
CACTTGCTGCTCCATGAGCC

am2CT/35
GAGGTCGAGCAGGCTGATGC

am2CT/42
TAGGTCGCGAGGTCGAGCAGG

am2CT/92
GTCCTTCTGCACCGAGTCGG

am1GA/49
CGCATCTTGTCTGGGTCAGG

am1GA/58
TCGTGAGGCGCATCTTGTCC

am45/1
ACGTGAGGTGGGTCTGTTCG

am45/96
GTAGCCTTCGGCATCCAGCG

am6TC/60
TCGGCATTGGGATAGTTGCGG

GI11/15
CCTCCTGTCTCATGCCGATGC

GI11/59
GCATTGCCCACGGAAGGAAGG

GI11/71
GAAGGCATCATGGCATTGCGC

GI18/62
GTCATGGGGTTTCCCAGAGACC

fliCa/41
GATCGCGATGTCGACGGTGCC

fliCa/42
CGATCGCGATGTCGACGGTGCC

fliCa/46
TGCCGATCGCGATGTCGACG

REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 17D

SG-1/40
GACGAATACCCAGCTGCGTGG

SG-1/43
GCAGACGAATACCCAGCTGCG

SG-4/1
CGCGACGTCGTGACGTCAGC

SG-4/67
ACTTTCGGCTCTTCGGGCTGG

TB46/21
AGGTAGAGACTCGGGGAACC

TB46/45
TCGTTTTCGGTCATGGCCAGG

TB471/22
TTCCGCGACGAACATCCGTGG

TB471/25
CGCTTCGCGACGAACATCCG

TB472/36
GGATCGCTTCCGATAGGGCAGC

TB472/84
AGAGGCATGGGTCTGTACCG

TB473/34
TCTGTCAATCCCCTTTGGGG

TB473/41
AGCCCCCTTCTGTCAATCCCC

TB474/36
GGCTTCCTACCGAAGGTCAGG

TB474/41
TGAGGGCTTCCTACCGAAGG

exoS/31
TTCAAGGTCATGGGCAATGCC

exoS/37
AGTCCCTTCAAGGTCATGGGC

exoU/22
GCCGACTGAGCTGTAGCTCGG

exoU/23
GGCCGACTGAGCTGTAGCTCG

exoU/42
ACCAGACTGGTCAATGGTGG

flins/2
CCCGTGTTTCCGTAGACCTTGC

pKL11/49a
AGCAGTTACCCACAGCATGG

REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 17E

pKL11/49b
CAGCAGTTACCCACAGCATGG

pKL3/47
CTACACTCCAACCGCTGGTCC

pKL3/50
GACCTACACTCCAACCGCTGG

pKL3/80
TTCCTTGCTGCCGAGAAGC

pKL7/14
TAATAGGCGAGCCTGCCGTCC

47D7nw1a
TCCACGCCGAGGGACGTGCC

47D7nw1b
GCTCCACGCCGAGGGACGTGCC

C46-nw1a
CGCGGTGCTGGTTGCGCTGC

C46-nw1b
CCAATGCCCAGGGCCAGCGGA

C46-nw1c
CGCTGGCAGTTCCGCTGGCC

ExoSnw1a
CAGGGTCGCCAGCTCGCTCGCC

ExoSnw1b
AGGGTCGCCAGCTCGCTCGC

ExoUnw1a
AGTGATCTGCCGCGGCCCTGCC

ExoUnw1b
GTGATCTGCCGCGGCCCTGC

OrfA-1
GTTCCACAGGCGCTGCGGCGC

OrfA-2
GTTCCACAGGCGCTGCGGCG

OrfA-3
CAAAGCCCCTGGTCGCGCGG

OrfC-1
GCAGCTTTTCCACCGCCGCGCGG

OrfI-1
AAACTGCCCCGCCCCCATCC

OrfI-2
GGAAAACTGCCCCGCCCCC

OrfJ-1
ACGCTCGCAGCGCCTCACGCG

REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 17F

OrfJ-2
GGCCTGGCTGCGAACGCTCGC

REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 18A

locus	name	5'-3'-sequence	group	length	GC-content [%]	Tm [°C]	spot-ID's
1	Pa-S_001	oriC T-C_wt					
2	Pa-S_003	oriC T-C_mut_1					
3	Pa-S_007	oprL T-C_wt_1					
4	Pa-S_010	oprL T-C_mut_1					
5	Pa-S_039	hcrA A-T_wt_1					
6	Pa-S_040	hcrA A-T_mut_1					
7	Pa-S_041	alkB2 G-A_wt_1					
8	Pa-S_042	alkB2 G-A_mut_1					
9	Pa-S_053	alkB2 A-G_wt_1					
10	Pa-S_064	alkB2 A-G_mut_1					
11	Pa-S_066	alkS A-G_wt_1					
12	Pa-S_066	alkS A-G_mut_1					
13	Pa-S_067	alkS G-C_wt_1					
14	Pa-S_068	alkS G-C_mut_1					
15	Pa-S_058	oprL T-C_wt_1					
16	Pa-S_070	oprL T-C_mut_1					
17	Pa-S_071	ampC_1 G-A_wt_1					
18	Pa-S_072	ampC_1 G-A_mut_1					
19	Pa-S_079	ampC_2 C-T_wt_1					
20	Pa-S_072	ampC_2 C-T_mut_1					
21	Pa-S_071	ampC_3 C-T_wt_1					
22	Pa-S_074	ampC_3 C-T_mut_1					
23	Pa-S_075	ampC_4 G-A_wt_1					
24	Pa-S_076	ampC_4 G-A_mut_1					
25	Pa-S_077	ampC_5 G-C_wt_1					

FIGURE 18B

16	Pa-S_026	ampC_5 G-	TGGAGCGGGAAGTGTTCCTCCGGC	1	22	63,6	65,8	66,67
17	Pa-S_027	ampC_6 T-C_wt	GAACAGAGACCGGTTCCACCAAGG	1	24	58,3	66,1	56,57
28	Pa-S_028	ampC_6 T-	AACAGAGACCGGTTCCACCAAGG	1	23	60,9	66,0	58,69
29	Pa-S_029	ampC_7 C-A_wt	GGACCGGCGGCTGGGATCCT	1	22	68,2	67,7	58,59
30	Pa-S_030	ampC_7 C-	GGACCGGCGGCTGGGATCCT	1	22	63,6	65,8	70,71
31	Pa-S_031	flhC b	GGCGACCACTGAACCTCACTCG	2	24	58,3	66,1	74,75
32	Pa-S_032	flhC a	GTGCGTGAACGGGCACTACTCA	2	23	56,5	64,2	66,87
33	Pa-S_033	exoS-1	CRGCTGGCGTCAATGTCCTCGG	3	22	68,2	67,7	76,77
34	Pa-S_034	exoU	CGCGAGTTTGAGAACGGAGTCAC	3	24	58,3	66,1	88,89
35	Pa-S_035	C-47-1	GGCGATCTTCTCCACTTCATCCG	4	24	54,2	64,4	78,79
36	Pa-S_036	C-47-2	GGCTCCGGCATTTGACATCGTGAT	4	24	58,3	66,1	90,91
37	Pa-S_040	47D7-1	GTAGCCGGAGTCGAGCGGATCAT	5	24	54,2	64,4	80,81
38	Pa-S_041	47D7-2	GTGAGCATGGAATCGGCGTCTGTT	5	24	58,3	66,1	92,93
39	Pa-S_054	C-45	CGAGGAGTTTCGGACCCGCTTGA	6	24	54,2	64,4	82,83
40	Pa-S_055	C-46	AATAGGACCGGCAACACGGGCATT	6	24	58,3	66,1	94,95
41	Pa-S_055	C-inselspez-4	GGGCTTCTCCCTCTATTCAGAGT	7	24	54,2	64,4	86,99
42	Pa-S_056	C-inselspez-5	CAGTATGGGACGGGACACGAGCGC	7	24	58,3	66,1	110,111
43	Pa-S_037	C-spezifisch-1	GCATCATTCGGCGTCACTCTGCT	8	24	58,3	66,1	122,123
44	Pa-S_044	pKL-3	TCTGATCTGGGGCTATCCCTGGA	9	24	54,2	64,4	100,101
45	Pa-S_045	pKL-7	AATTGATGGCTTCTCAGGGCGAGG	9	24	54,2	64,4	112,113
46	Pa-S_046	pKL-11	AGTCATGGGACTGATACGGGCGACT	9	25	52,0	64,6	124,125
47	Pa-S_042	PAGI-1-1	TTCTCGGTGTCGAGGGGATCTCGG	10	24	58,3	66,1	102,103
48	Pa-S_043	PAGI-1-5	TGGTACCTCTCGACGTACTGGCTG	10	24	58,3	66,1	114,115
49	Pa-S_047	SG17M-1	CCCGTTGGCTATACCGGTTCTG	11	24	58,3	66,1	104,105
50	Pa-S_046	SG17M-4	AGGCGATTCTCAGGTGGACTCAGG	11	24	54,2	64,4	116,117
51	Pa-S_053	fla-insel-1	ACCTGTGTCGGTGGGCGGATGTT	12	24	58,3	66,1	106,107
52	Pa-S_049	TB-C47-1	AGGTCCCTGACCACTCATCAG	13	24	58,3	66,1	118,119
53	Pa-S_050	TB-C47-2	CGCCACCAATTGGCCATTACAGCG	13	24	54,2	64,4	126,127
54	Pa-S_051	TB-C47-3	TCCAAACAGGAGGATACAGGGTG	13	24	58,3	66,1	128,129

FIGURE 18C

55	Pa-S_052	TB-C47-4	CGCTGCACATACAGGTCGGTTCTC	13	24	54,2	64,4	130,131
56	Biotin + Cy3-marker							1,12,97,121,132
57	Pa-S_081	oriC T-C_wt_1	AGCCCAGCAATTCGGTGTTCCTCCG	1	25	65,6	56	
58	Pa-S_082	oriC T-C_mut_2	AGCCCAGCAACTGCGTGTTCCTCC	1	24	65,1	58	
59	Pa-S_083	alkB2 G-A_wt_2	GCTGCTGGCGCGGTGTGC		19	67,4	79	8,9
60	Pa-S_084	alkB2 G-A_mut_2	TGCTGCTGGCAGCGGTGTGCT		21	67,3	67	20,21
61	Pa-S_085	oprI T-C_wt_2	CAGAAAGCTCAGCAGACTGCTGACGAG		27	64,6	56	
62	Pa-S_086	oprI T-C_mut_2	GAAAGCTCAGCAGACCGCTGACGAG		25	64,9	60	
63	Pa-S_087	ampC_1 G-A_wt_2	ACGGCCGCCGGGTGACGCC		19	70,2	84	
	ampC_1 G-							
64	Pa-S_088	A_mut_2	ACGGCCGCCAGGTGACGCCG		20	69,9	80	
65	Pa-S_089	ampC_3 C-T_wt_1	GCCGACCTACGCCCGCCGGC		19	68,4	84	
	ampC_3 C-							
66	Pa-S_090	T_mut_2	AGCCGACCTATGCCCGCGGGCA		21	68,4	71	
67	Pa-S_091	ampC_4 G-A_wt_2	GTTCGAACGGCTCATGGAGCAGCA		24	65	58	
	ampC_4 G-							
68	Pa-S_092	A_mut_2	GTTCGAACGACTCATGGAGCAGCAAG		26	63,5	54	
69	Pa-S_093	exoS-1_1	CAGCCAGTCAGGACGCCGA		20	64,9	70	
70	Pa-S_094	exoU_1	AGTGACGTGCGTTTCAGCAGTCCC		24	64,8	58	
71	Pa-S_095	47D7-1_1	GTGTACGGGCCCATGTCTAGCAGC		24	65	63	
72	Pa-S_096	C-46_1	CGAAGTCTGAGGTGTGGACCCGC		23	64,5	65	
73	Pa-S_097	Fla-Insel-2_orfA	CGCTGGAGGGTATGTTCGCAAGG		24	64,8	63	
74	Pa-S_098	Fla-Insel-2_orfC	CGTACTCAGCTTCTCCACCCAGCG		24	64,3	63	
75	Pa-S_099	Fla-Insel-2_orfI	CCTGGACCTCTCCAAGGTTGCGCT		24	65	63	
76	Pa-S_100	Fla-Insel-2_orfJ	GCCATTCCGACGACCAAAACAAGGC		24	64,2	58	

group "mother"

FIGURE 19A

seq- id	seq	name	5'-3'-sequence	group	length	GC- content [%]	Tm [°C]	spot- ID's
1	Pa-S_001	oriC T-C_wt	GAAGCCAGGCAATTGGCGTGTTC	1	23	52,2	62,4	23
2	Pa-S_002	oriC T-C_mut_1	GAAGCCAGGCAACTGGGTGTTC	1	23	56,5	64,2	14,15
3	Pa-S_003	oriC T-C_wt_1	AGCCAGGCAATTGGGTGTTC	1	25	65,6	56	13,25
4	Pa-S_004	oriC T-C_mut_2	AGCCAGGCAATCGGGTGTTC	1	24	65,1	58	37,49
5	Pa-S_005	oriC T-C_wt_1	GTTGCTGCAAGGTGTTC	1	23	69,6	69,6	4,5
6	Pa-S_006	oriC T-C_mut_1	GTTGCTGCAAGCGGTTC	1	23	73,9	71,3	16,17
7	Pa-S_007	oriC A-T_wt_1	CAAGATGCCCCAAGCGGTAC	1	22	63,6	65,8	6,7
8	Pa-S_008	oriC A-T_mut_1	CAAGATGCCCCGCTGCGGTAC	1	22	63,6	65,8	18,19
9	Pa-S_009	oriC G-A_wt_2	GCTGCTGGCGCGGTGTC	1	19	67,4	79	8,9
10	Pa-S_010	oriC G-A_mut_2	TGCTGCTGGCGCGGTGTC	1	21	67,3	67	20,21
11	Pa-S_011	oriC A-G_wt_1	CCTGCCCCGTTCACCGGTCTGG	1	25	72,0	72,8	10,11
12	Pa-S_012	oriC A-G_wt_1	CTCGCCCTGTTCGCGGTCTGG	1	24	75,0	73,0	22,23
13	Pa-S_013	oriC A-G_wt_1	TCGAGCACTGGCGAGGATACCG	1	24	54,2	64,4	26,27
14	Pa-S_014	oriC G-C_wt_1	CGAGCACTGGCGAGGATACCG	1	23	60,9	66,0	38,39
15	Pa-S_015	oriC G-C_wt_1	ACGGAACCTTCCTGCAATGATGT	1	26	46,2	63,2	28,29
16	Pa-S_016	oriC T-C_wt_1	GCGGAACTTCCTGCAATGATGT	1	26	46,2	63,2	40,41
17	Pa-S_017	oriC T-C_wt_1	AGCTCAGCGACTGCTGACGAGG	1	23	60,9	66,0	30,31
18	Pa-S_018	oriC T-C_wt_1	AGCTCAGCGACTGCTGACGAGG	1	22	63,6	65,8	42,43
19	Pa-S_019	oriC T-C_wt_2	CAGGAGCTCGCGACTGCTGACGAG	1	27	64,6	56	61,73
20	Pa-S_020	oriC T-C_wt_2	GAGGAGCTCGCGACTGCTGACGAG	1	25	64,9	60	24,85
21	Pa-S_021	oriC T-C_wt_2	ACGSCCGCGCGGTGACGCC	1	19	70,2	84	32,33
22	Pa-S_022	oriC T-C_wt_2	ACGSCCGCGCGGTGACGCC	1	20	69,9	80	44,45
23	Pa-S_023	oriC T-C_wt_2	GACAGATGGCGCTCGACGAC	1	22	63,6	65,8	34,35
24	Pa-S_024	oriC T-C_wt_2	GACAGATGGCGCTCGACGAC	1	23	60,9	66,0	46,47
25	Pa-S_025	oriC T-C_wt_2	ACCCGACCTACGGCGCGGCGAG	1	22	77,3	71,4	50,51
26	Pa-S_026	oriC T-C_wt_2	CAGCCGACCTACGGCGCGGCGAG	1	23	73,9	71,3	62,63

FIGURE 19B

65	Pa-S_059	ampC_3 C-T_wt_1	GCCGACCTACGGCGCGGGG	1	19	68,4	84	36,48
66	Pa-S_060	ampC_3 C-T_mut_2	AACCGACCTATGCGCGCGGGCA	1	21	68,4	71	60,72
67	Pa-S_061	ampC_4 G-A_wt_2	GTTCGACGCGCTCATGGAGCAGCA	1	24	65	58	52,53
68	Pa-S_062	ampC_4 G-A_mut_2	GTTCGACGCGCTCATGGAGCAGCAAG	1	26	63,5	54	64,65
69	Pa-S_077	ampC_5 G-C_wt_1	TCGAGCGACGAGTGTTCGCGGGC	1	22	63,6	65,8	54,55
70	Pa-S_078	ampC_5 G-C-T_mut_1	TGGAGCGACGCACTGTTCGCGGGC	1	22	63,6	65,8	66,67
71	Pa-S_027	ampC_6 T-C_wt	GAACGAGACCGGTTCCACCAAGG	1	24	58,3	66,1	55,57
72	Pa-S_079	ampC_6 T-C-T_mut_1	AACGAGACCGGCTCCACCAAGG	1	23	60,9	66,0	68,69
73	Pa-S_029	ampC_7 C-A_wt	GCGACCTCGGCGCTGTCGATCCT	1	22	68,2	67,7	58,59
74	Pa-S_080	ampC_7 C-A-T_mut_1	GCGACCTCGGCGCTGTCGATCCT	1	22	63,6	65,8	70,71
75	Pa-S_031	flic b	GCGGCGCACTGCTCTCCACTCG	2	24	58,3	66,1	74,75
76	Pa-S_032	huc a	GTGGCGTGAACGGGACCTACTTCA	2	23	56,5	64,2	86,87
77	Pa-S_033	exoS-1_1	CAGCGGAGTCAAGGCGCGGGA	3	20	64,9	50	76,77
78	Pa-S_034	exu	GCGCAGTTCGAGACGCGAGTCACC	3	24	58,3	66,1	88,89
79	Pa-S_034	exuU_1	AGTCAGTTCGCTTCGCGGTCCC	3	24	64,8	58	84,85
80	Pa-S_035	C-47-1	GCGCGTCTTCTCCACTTCACTCG	4	24	54,2	64,4	78,79
81	Pa-S_035	47D7-1_1	GTGTCACGGCCCATGTCTAGCAGC	5	24	65	63	80,81
82	Pa-S_034	47D7-2	GTGAGCATGGATCCGGCAGTCGTT	5	24	58,3	66,1	92,93
83	Pa-S_054	C-45	CGACGCTTTCGGACCGGCTTTGA	6	24	54,2	64,4	82,83
84	Pa-S_055	C-46	AATAGGACCGGCGACGACGGGCATT	6	24	58,3	66,1	94,95
85	Pa-S_056	C-48_1	CGAAGTCGTGAGGTGTGACCCGC	6	23	64,5	65	108,120
86	Pa-S_035	C-Inselspez-4	GCGCCCTCTCCTCTTTCAGATGT	7	24	54,2	64,4	98,99
87	Pa-S_036	C-Inselspez-5	CACTATGCTACCGACACGACGCGC	7	24	58,3	66,1	110,111
88	Pa-S_037	C-spezifisch-1	GCATCATTTGCGCGTCACATCTGGT	8	24	58,3	66,1	122,123
89	Pa-S_044	pKL-3	TCTGAATCGGGGTATCACCTGGT	9	24	54,2	64,4	100,101
90	Pa-S_045	pKL-11	AGTCATGCGGACTGATACCGCGGACT	9	25	52,0	64,6	124,125
91	Pa-S_042	PAGI-1-1	TTCTCGGTGTCGAGGGAATCTCGG	10	24	58,3	66,1	102,103
92	Pa-S_043	PAGI-1-8	TGGTAGCTCTCGACGTACTCGCTG	10	24	58,3	66,1	114,115

FIGURE 19C

49	Pa-S_047	SG17M-1	CCCGTTGCTCATACCCGGTCCCTG	11	24	58,3	66,1	104,105
50	Pa-S_048	SG17M-4	AGGSCATTTCTCAGGTGGACICAGG	11	24	54,2	64,4	116,117
51	Pa-S_050	fla-insel-1	ACCGGTGTGGCTGGAGGGTATGTT	12	24	58,3	66,1	108,107
52	Pa-S_051	TB-C47-3	TCCATCAGGCGGGGTACAGGGTG	13	24	58,3	66,1	128,129
53	Pa-S_052	TB-C47-4	CGCAGCATACAGGTCCCTTCTC	13	24	54,2	64,4	130,131
73	Pa-S_037	Fla-Insel-2_orfA	CGCTGGAGGGTATCTTCGGCAGG	14	24	64,8	63	90,91
74	Pa-S_038	Fla-Insel-2_orfC	CGTACTCAGCTTCTCCACCCAGGG	14	24	64,3	63	112,113
75	Pa-S_039	Pa-Insel-2_orfI	CCCTGGACCTTCTCCAGGGTTCGCCCT	14	24	65	63	118,119
76	Pa-S_100	Fla-Insel-2_orfJ	GCCATTCCGACGACCCAAACAGGC	14	24	64,2	58	126,127
56	Blau + O_2-marker							1,12,97,121,132

Group "mother"

FIGURE 20

Chip: MHH_P_aer_array2 (12x11 array with spot distance of 19.00 mm)

56	43	43	46	46	76	76	54	54	55	55	56
	42	42	74	74	48	48	50	50	75	75	72
56	41	41	44	44	47	47	49	49	51	51	72
62	32	32	34	34	73	73	38	38	40	40	70
61	31	31	69	69	35	35	71	71	39	39	70
61	22	22	68	68	26	26	28	28	30	30	66
58	21	21	67	67	25	25	27	27	29	29	66
58	12	12	14	14	16	16	64	64	20	20	65
57	11	11	13	13	15	15	63	63	19	19	65
57	2	2	4	4	6	6	60	60	10	10	62
56	1	1	3	3	5	5	59	59	9	9	56

FIGURE 21

Chip occupancy

marker spot	C-spezifisch-1	pKL-11	Fla-Insel-2_orfJ	TB-C47-3	TB-C47-4	marker spot
mut_2 oprL T-C wt_2 oprL T-C wt_2	C-Insel-spezifisch-5 flic A	Fla-Insel-2_orfC	PAGI-1-8	SG17M-4	Fla-Insel-2_orfI	C-46_1
		pKL-3	PAGI-1-1	SG17M-1	fla-Insel-1	C-46_1
mut_2 oprL T-C wt_2 oprL T-C wt_2	flic B	exoU	Fla-Insel-2_orfA	47D7-2	C-46	exoU_1
		exoS-1_1	C-47-1	47D7-1_1	C-45	exoU_1
mut_2 oriC T-C wt_2 oprL T-C wt_1 oprL T-C wt_1	mut_1 ampC_3 C-T wt	mut_2 ampC_4 G-A wt_2	mut_1 ampC_5 G-C wt_1	mut_1 ampC_6 T-C wt	mut_1 ampC_7 C-A wt	mut_2 ampC_3 C-T mut_2 ampC_3 C-T wt_1 ampC_3 C-T wt_1
		mut_1 citS A-G wt_1	mut_1 oprL T-C wt_1	mut_2 ampC_1 G-A wt_2	mut_1 ampC_2 C-T wt	
mut_2 oriC T-C wt_1	mut_1 oriC T-C wt	mut_1 oprL T-C wt_1	mut_1 flic a A-T wt_1	mut_2 alkB2 G-A wt_2	mut_1 alkB2 A-G wt_1	oprL T-C mut_2 marker spot